

Table IV. HLA Class I Standard Peptide Binding Affinity.

ALLELE	STANDARD PEPTIDE	SEQUENCE	SEQ ID NO:	STANDARD BINDING AFFINITY (nM)
A*0101	944.02	YLEPAIAKY	1189	25
A*0201	941.01	FLPSDYFPSV	1190	5.0
A*0202	941.01	FLPSDYFPSV	1191	4.3
A*0203	941.01	FLPSDYFPSV	1192	10
A*0205	941.01	FLPSDYFPSV	1193	4.3
A*0206	941.01	FLPSDYFPSV	1194	3.7
A*0207	941.01	FLPSDYFPSV	1195	23
A*6802	1072.34	YVIKVSARV	1196	8.0
A*0301	941.12	KVFPYALINK	1197	11
A*1101	940.06	AVDLYHFLK	1198	6.0
A*3101	941.12	KVFPYALINK	1199	18
A*3301	1083.02	STLPETYVRR	1200	29
A*6801	941.12	KVFPYALINK	1201	8.0
A*2402	979.02	AYIDNYNKF	1202	12
B*0702	1075.23	APRTLVL	1203	5.5
B*3501	1021.05	FPFKYAAAF	1204	7.2
B51	1021.05	FPFKYAAAF	1205	5.5
B*5301	1021.05	FPFKYAAAF	1206	9.3
B*5401	1021.05	FPFKYAAAF	1207	10

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Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	Sequence	SEQ ID NO:	Binding Affinity (nM)
DRB1*0101	DR1	515.01	PKYVKQNTLKLAT	1208	5.0
DRB1*0301	DR3	829.02	YKTIAFDEEARR	1209	300
DRB1*0401	DR4w4	515.01	PKYVKQNTLKLAT	1210	45
DRB1*0404	DR4w14	717.01	YARFQSQTTLKQKT	1211	50
DRB1*0405	DR4w15	717.01	YARFQSQTTLKQKT	1212	38
DRB1*0701	DR7	553.01	QYIKANSKFIGITE	1213	25
DRB1*0802	DR8w2	553.01	QYIKANSKFIGITE	1214	49
DRB1*0803	DR8w3	553.01	QYIKANSKFIGITE	1215	1600
DRB1*0901	DR9	553.01	QYIKANSKFIGITE	1216	75
DRB1*1101	DR5w11	553.01	QYIKANSKFIGITE	1217	20
DRB1*1201	DR5w12	1200.05	EALIHQLKINPYVLS	1218	298
DRB1*1302	DR6w19	650.22	QYIKANAKFIGITE	1219	3.5
DRB1*1501	DR2w2 $\beta$ 1	507.02	GRTQDENPVVHFFKNIVTP RTPPP	1220	9.1
DRB3*0101	DR52a	511	NGQIGNDPNRDIL	1221	470
DRB4*0101	DRw53	717.01	YARFQSQTTLKQKT	1222	58
DRB5*0101	DR2w2 $\beta$ 2	553.01	QYIKANSKFIGITE	1223	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

Table XIX p53 DR Super Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2wβ1	DR2w2β2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
VTCTYSPAL	1123	AKSVTCYSPALNKM	1057	119								
LKDAQAGKE	1124	ALELKDAQAGKEPGG	1058	347								
VAPAPAPT	1125	APPVAPAPAPTAA	1059	70								
MPEAAPVA	1126	APRMPEAAPVAPAP	1060	63								
WPLSSVPS	1127	APSWPLSSVPSQKT	1061	88								
IHYNYMCS	1128	CTTHYNYMCSNCSM	1062	229								
YFTLQIRGR	1129	DGEYFTLQIRGRF	1063	324					-0.0027			
LSPDDIEOW	1130	DLMLSPDDIEOWFTE	1064	42	0.0400			0.0150				
VEPLSQET	1131	DPSEPLSQETFS	1065	7				0.0039				
LRVEYLDLR	1132	EGLRVEYLDLRNIF	1066	198								
VLSPLSQQA	1133	ENNVLSPLSQQAMDD	1067	28								
LAKTCPVOL	1134	FCQLAKTCPVOLWVD	1068	134								
LWKLLPEN	1135	FSDLWKLLPENNVLS	1069	19								
LGFLHSGTA	1136	GFRLGFLHSGTAKSV	1070	108	1.9000	0.0360	0.1200	0.0027	8.3000		0.2000	
VRAMAIYKQ	1137	GTRVAMAIYKQSQH	1071	154								
LPFGSTKRA	1138	HHELPFGSTKRALPN	1072	296								
VVPYEPVEV	1139	HSVVVPYEPVEVGS	1073	214								
YMCNSSCMG	1140	HYNYMCSNCSMGGMN	1074	233								
WFTEDPGPD	1141	IEQWFTEDPGPDEAP	1075	50	-0.0005							
LPNTSSSP	1142	KRALPNNTSSSPQPK	1076	305								
LHSGTAKSV	1143	LGLHSGTAKSVTCT	1077	111								
MFCOLAKTC	1144	LNMFCOLAKTCPVQ	1078	130	0.2500	0.0016	0.0370	0.0006	0.0560		0.0080	
LPSQAMDDL	1145	LSPLSQAMDDLMLS	1079	32								
ITLEDSSGN	1146	LTITLEDSSGNLLG	1080	252				0.0030				
MNRRLTI	1147	MGMNRRLTIITL	1081	243	-0.0005				-0.0027			
VVRCPHHE	1148	MTEVVRCPHHERCS	1082	169								
LELKDAQAG	1149	NEALELKDAQAGKEP	1083	345								
LSPLSQAM	1150	NNVLSPLSQAMDDL	1084	29								
IEQWFTEDP	1151	PDDIEQWFTEDPGPD	1085	47								
VGSDCTTH	1152	PPEVGSDDCTTHYNY	1086	222								
LWVDSTPPP	1153	PVQLWVDSTPPGTR	1087	142								
VDSTPPPGT	1154	QLWVDSTPPPGTRVR	1088	144								
FLHSGTAKS	1155	RLGFLHSGTAKSVTC	1089	110				0.0380				
FEVRVCACP	1156	RNSFEVRVCACPGRD	1090	267				0.0300				
FRHSVVVPY	1157	RNTRHSVVVPYEP	1091	209								
LTITLED	1158	RPILTITLEDSSGN	1092	249								
ILTITLED	1159	RRPILTITLEDSSG	1093	248	0.0010				0.0100			
VRVCACPGR	1160	SFEVRVCACPGRDRR	1094	269								
LLGRNSFEV	1161	SGNLLGRNSFEVRVC	1095	261								
LNMFCOLA	1162	SPALNKMFCOLAKTC	1096	127								
MDLMLSPD	1163	SQAMDDLMLSPDDIE	1097	37								
VPSOKTYOG	1164	SSVPSOKTYOGSYG	1098	94								
VPEPVEVG	1165	SVVVPYEPVEVGSDC	1099	215								
LSSVPSQK	1166	SWPLSSVPSQKTYQ	1100	90								
FRGLHSG	1167	SYGFRGLHSGTAK	1101	106								
LDDRNTRFH	1168	VEYLDNRNTRFHSV	1102	203								
WDDSTPPPG	1169	VQLWVDSTPPPGTRV	1103	143								
YEPPEVGS	1170	VVPYEPPEVGSDDCT	1104	217								
LPENNVLSP	1171	WKLLPENNVLSPLS	1105	23								
MCNSSCMGG	1172	YNYMCSNCSMGGMNR	1106	234								

Table XIX p53 DR Super Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9
VTCTYSPAL	1123	AKSVTCTYSPALNKM	1057				
LKDAQAGKE	1124	ALELKDAQAGKERGG	1058				
VAPAPAAPT	1125	APVAPAPAAPTPAA	1059				
MPEAAPPA	1126	APRMPEAAPPAAPAP	1060				
WPLSSSVPS	1127	APSWPLSSSVPSQKT	1061				
IHYNYMCNS	1128	CTTHYNYMCNSSCM	1062				
YFTLQIRGR	1129	DGEYFTLQIRGRERF	1063		-0.0018		
LSPDIEQW	1130	DLMLSPDIEQWFTF	1064				
VEPLSQET	1131	DFSVEPLSQETFS	1065				
LRVEYLLDR	1132	EGNLRVEYLLDRNTF	1066				
VLSPLSQA	1133	ENNVLSPLSQAMDD	1067				
LAKTCPVQL	1134	FCQLAKTCPVQLWVD	1068				
LWKLLENN	1135	FSDLWKLLENNVLS	1069				
LGLHSGTA	1136	GFLGLHSGTAKSV	1070	0.0460	0.2800	1.7000	
VRAMAIYKQ	1137	GTRVRAMAIYKQSQH	1071				
LPPGSTKRA	1138	HHELPPGSTKRALPN	1072				
VVPYEPEV	1139	HSVVVPEPEVPGSD	1073				
YMCNSSCMG	1140	HYNYMCNSSCMGGMN	1074				
WFTEDPGPD	1141	IEQWFTEDPGDEAP	1075		-0.0007		
LPNNTSSP	1142	KRALPNNTSSSPQPK	1076				
LHSGTAKSV	1143	LGLHSGTAKSVTCT	1077				
MFCQLAKTC	1144	LNMFCQLAKTCVPQ	1078	0.0096	0.1500	0.0320	
LPSQAMDDL	1145	LSPLSQAMDDLMLS	1079				
ITLEDSSGN	1146	LTITLEDSSGNLLG	1080				
MNRRPILTI	1147	MGMNRRPILTIITL	1081		-0.0007		
VVRCRPHHE	1148	MTEVVRCRPHHERCS	1082				
LELKDAOAG	1149	NEALELKDAOAGKEP	1083				
LSPLSQAM	1150	NNVLSPLSQAMDDL	1084				
IEQWFTEDP	1151	PDDIEQWFTEDPGD	1085				
VGSDCTTH	1152	PPEVGSDCTTHYNY	1086				
LWVDSTPPP	1153	PVQLWVDSTPPPGR	1087				
VDSTPPPGT	1154	QLWVDSTPPPGRVR	1088				
FLHSGTAKS	1155	RLGLHSGTAKSVTC	1089				
FEVRVCACP	1156	RNSEVRVCACPGRD	1090				
FRHSVVVPY	1157	RNIFRHSVVVPYEP	1091				
LTITLED	1158	RPILTIITLEDSSGN	1092				
ILTIITLED	1159	RRPILTIITLEDSSG	1093		0.0023		
VRVCACPGR	1160	SFEVRVCACPGRDR	1094				
LLGRNSFEV	1161	SGNLGRNSFEVRVC	1095				
LNKMFQCLA	1162	SPALNKMFQCLAKTC	1096				
MDDLMLSPD	1163	SQAMDDLMLSPDDIE	1097				
VPSQKTYQG	1164	SSSVPSQKTYQGSYG	1098				
VPEPEPEV	1165	SVVPEPEPEVGSDC	1099				
LSSSVPSQK	1166	SWPLSSSVPSQKTYQ	1100				
FRLGFLHSG	1167	SYGFRGLGFLHSGTAK	1101				
LDDRNIFRH	1168	VEYLLDDRNIFRHSVV	1102				
WVDSTPPPG	1169	VQLWVDSTPPPGTIRV	1103				
YEPPEVGS	1170	VVPPEPEVGSDCCT	1104				
LPENNVLSP	1171	WKLLENNVLSPLPS	1105				
MCNSSCMGG	1172	YNYMCNSSCMGGMNR	1106				

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Cont.

Table XXa p53 DR 3a Motif Peptides with Binding Data

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Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w2B1	DR2w2B2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LSPDDIEQW	1173	DLMLSPDDIEQWFTF	1107	42				0.0150				
LRVEYLDDR	1174	EGNLRVEYLDDRNTF	1108	198				0.0039				
LSQETFSDL	1175	EPPLSQETFSDLWKL	1109	11				-0.0025				
FTEDPGPDE	1176	EQWFTEDPGPDEAPR	1110	51				-0.0025				
LDGEVFTLQ	1177	KKPLDGEVFTLQIRG	1111	320				-0.0025				
ITLEDSSGN	1178	LTITLEDSSGNLLG	1112	252				0.0030				
LJPENNVL	1179	LWKLLPENNVLSPLP	1113	22				0.0029				
VGSDCTTH	1180	PPEVGSDCCTTHYNY	1114	222				0.0380				
LWVDSTPPP	1181	PVQLWVDSTPPPGTR	1115	142				0.0300				
IRVEGNLRV	1182	QHLIRVEGNLRVEYL	1116	192				0.0960				
MFRELNEAL	1183	RFEMFRELNEALELK	1117	337				0.0052				
YLDDRNTR	1184	RVEYLDDRNTRFRHSV	1118	202				0.1800				
VPYEPPEVG	1185	SVVVPYEPPEVGSDC	1119	215				-0.0025				

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Conf.

Table XXa p53 DR 3a Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LSPDDIEOW	1173	DLMSPDDIEQWTFE	1107					
LRVEYLDNR	1174	EGNLRVEYLDNRNTF	1108					
LSOETFSDL	1175	EPPLSQETFSDLWKL	1109					
FTEDPGPDE	1176	EQWFTEDPGPDEAPR	1110					
LDGEVFTLQ	1177	KKPLDGEYFTLQIRG	1111					
ITLEDSSGN	1178	LTHILEDSSGNLLG	1112					
LLPENNVL	1179	LWKLLPENNVLSPLP	1113					
VGSDCTTH	1180	PPEVGSDCTTHYNY	1114					
LWVDSTPPP	1181	PVQLWVDSTPPPGTR	1115					
IRVEGNLRV	1182	QHLIRVEGNLRVEYL	1116					
MFRELNEAL	1183	RFEMFRELNEALELK	1117					
YLDNRNTR	1184	RVEYLDNRNTRHSV	1118					
VPYEPPEVG	1185	SVVVPYEPPEVGSDC	1119					

AS  
conf

Table XXb p53 DR 3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w2B1	DR2w2B2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
FTLQIRGRE	1186	GEYFTLQIRGRERFE	1120	325				0.0290				
VEGNLRVEY	1187	LIRVEGNLRVEYLLDD	1121	194				0.0930				
YKQSQHMT	1188	MAIYKQSQHMTVEVVR	1122	160				-0.0025				


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conclude

Table XXb p53 DR 3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
FTLQIRGRE	1186	GEYFTLQIRGRERFE	1120					
VEGNLRVEY	1187	LIRVEGNLRVEYLDD	1121					
YKQSQHMT	1188	MAIYKQSQHMTVEVVR	1122					




Table XXII. A2 supermotif analogs



Source	AA	Sequence	SEQ ID NO:	A*0201 nM
p53.24	9	KLLPENNVVL	1224	313
p53.24V9	9	KLLPENNVV	1225	385
p53.25	11	LLPENNVLSPL	1226	19
p53.25V9	11	LLPENNVLSPV	1227	39
p53.65	9	RMPEAAPPV	1228	119
p53.65L2	9	RLPEAAPPV	1229	78
p53.65	10	RMPEAAPVA	1230	78
p53.65L2V10	10	RLPEAAPVV	1231	143
p53.65M2V10	10	RMPEAAPVV	1232	54
p53.69	8	AAPPVAPA	1233	5000
p53.69L2V8	8	ALPPVAPV	1234	217
p53.101	11	KTYQGSYGFR	1235	1786
p53.101L2V11	11	KLYQGSYGFRV	1236	81
p53.113	11	FLHSGTAKSVT	1237	5000
p53.113V11	11	FLHSGTAKSVV	1238	1220
p53.129	9	ALNKMFCQL	1239	735
p53.129V9	9	ALNKMFCQV	1240	75
p53.129B7V9	9	ALNKMFBQV	1241	192
p53.129	10	ALNKMFCQLA	1242	1316
p53.129V10	10	ALNKMFCQLV	1243	217
p53.132	9	KMFCQLAKT	1244	333
p53.132V9	9	KMFCQLAKV	1245	33
p53.132B4V9	9	KMFBQLAKV	1246	125
p53.132L2V9	9	KLFCQLAKV	1247	98
p53.135	9	CQLAKTCPV	1248	208
p53.135L2	9	CLLAKTCPV	1249	125
p53.135B1B7	9	BQLAKTBPV	1250	102
p53.135B1L2B7	9	BLLAKTBPV	1251	46
p53.139	9	KTCPVQLWV	1252	725
p53.139L2	9	KLCPVQLWV	1253	122
p53.139L2B3	9	KLBPVQLWV	1254	46
p53.149	9	STPPPGTRV	1255	909
p53.149M2	9	SMPPPGTRV	1256	172
p53.149L2	9	SLPPPGTRV	1257	122
p53.164	9	KQSQHMTEV	1258	500
p53.164L2	9	KLSQHMTEV	1259	122
p53.216	10	VVVPYEPPEV	1260	617
p53.216L2	10	VLVPYEPPEV	1261	89
p53.229	9	CTTIHYNM	1262	278
p53.229L2V9	9	CLTIHYNV	1263	263
p53.229B1L2V9	9	BLTIHYNV	1264	116
p53.236	8	YMCNSSCM	1265	4546
p53.236L2M8	8	YLCNSSCV	1266	--
p53.236	11	YMCNSSCMGGM	1267	667
p53.236L2M11	11	YLCNSSCMGGV	1268	22
p53.255	11	ITLEDSSGNLL	1269	1563
p53.255L2V11	11	ILLEDSSGNLV	1270	33
p53.256	10	TLEDSSGNLL	1271	1667
p53.256V10	10	TLEDSSGNLV	1272	4167

Table XXIIA A01 Analog Peptides



<u>Peptide</u>	<u>AA</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>A*0101 nM</u>
52.0136	11	GSDCTTIHYN	1273	p53.226	67.6
57.0035	9	GTDCTTIHY	1274	p53.226.T2	0.9
57.0125	10	PTQKTYQGSY	1275	p53.98.T2	35.7
57.0126	10	GTDKSVTCTY	1276	p53.117.D3	42.4
57.0127	10	RVDGNLRVEY	1277	p53.196.D3	45.5


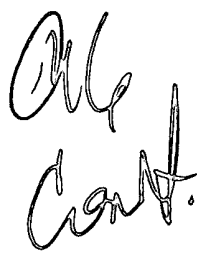


Table XXII B A03 Analog Peptides

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Peptide	AA	Sequence	SEQ ID NO:	Source	A*0301 nM	A*1101 nM	A*3101 nM	A*3301 nM	A*6801 nM	A3 XRN
1371.14	10	KVYQGSYGFR	1278	p53.101.V2	37.9	61.9	72	10000	40	4
1371.15	10	KVYQGSYGFK	1279	p53.101.V2K10	33.3	9.2	138.5	-72500	38.1	4
1371.16	9	BVYSPALNK	1280	p53.124.B1V2	15.7	12.8	439	22307.7	500	4
1371.17	9	BVYSPALNR	1281	p53.124.B1V2R9	25	8.3	33.3	85.3	14.8	5
1371.18	8	KVFBQLAK	1282	p53.132.V2B4	846.2	461.5	7500	-72500	8888.9	1
1371.2	11	GVRVRAIAIYK	1283	p53.154.V2	57.9	136.4	418.6	-72500	13333.3	3
1371.22	9	RVRAMAIYR	1284	p53.156.R9	40.7	1666.7	8.6	138.1	666.7	3
1371.24	9	SVBMGGMNK	1285	p53.240.V2B3K9	12.5	17.1	9000	-72500	29.6	3
1371.25	10	SVBMGGMNRK	1286	p53.240.V2B3K10	100	75	-36000	-72500	17	3
1371.26	9	SVBMGGMNR	1287	p53.240.V2B3	161.8	95.2	120	852.9	11.1	4
1371.27	10	SVBMGGMNR	1288	p53.240.V2B3	1000	25	620.7	805.6	11.4	2
1371.31	11	RVBABPGDRDK	1289	p53.273.B3B5K11	314.3	200	4615.4	-72500	2500	2
1371.32	11	SVSRHKLMFK	1290	p53.376.V2	33.3	54.5	295.1	18125	1509.4	3
1371.33	11	SVSRHKLMFR	1291	p53.376.V2R11	196.4	2857.1	183.7	1381	500	3

Table XXII C A02 Analog Peptides



Peptide	AA	Sequence	SEQ ID NO:	Source	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	A2 XRN
27.0068	9	KMFCQLAKT	1292	p53.132	505.1	14.3	19.6	92.5	-40000	3
39.0074	9	LLGRDSFEV	1293	mp53.261	41.7					
44.0003	9	LLGRDSFEV	1294	mp53.261	27.8					
1317.22	9	ALNKMFCQL	1295	p53.129	735.3	390.9	18.5	72.5	-80000	3
1317.23	9	KMFCQLAKT	1296	p53.132	333.3	33.1	17.5	105.7	-80000	4
1324.08	9	KQSQHMTEV	1297	p53.164	500	130.3	169.5	284.6	-80000	4
1329.04	9	CTTIHNYM	1298	p53.229	277.8	286.7	2564.1	560.6	181.8	3
1329.07	9	KLLPENNVL	1299	p53.24	312.5	1954.5	12500	1193.5	-80000	1
1329.09	10	FLHSGTAKSV	1300	p53.113	357.1	179.2	14.5	4625	80000	3

Table XXIID A24 Analog Peptides



<u>Peptide</u>	<u>AA</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>A*2401 nM</u>
52.008	8	TYQGSYGF	1301	p53.102	109.1
52.0081	8	SYGFRLGF	1302	p53.106	428.6
52.0103	10	TYQGSYGFRL	1303	p53.102	100
52.0104	10	TYSPALNKMF	1304	p53.125	2.4
52.0144	11	TYLWWVNNQSL	1305	CEA.353	46.2
52.0147	11	TYLWWVNGQSL	1306	CEA.531	92.3
57.0042	9	LYWVNGQSF	1307	CEA.533.Y2F9	15.8
57.0051	9	EYVNARHCF	1308	Her2/neu.553.F9	150
57.007	9	TYSDLWKLF	1309	p53.18.Y2F9	5.5
57.0071	9	SYGFRLGFF	1310	p53.106.F9	121.2
57.0096	10	TYQGSYGFRF	1311	p53.102.F10	30

TABLE XXIIE B07 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	B*0702 nM	B*3501 nM	B*5101 nM	B*5301 nM	B*5401 nM	B7 XRN
48.0055	8	FPALNKMIF	1312	p53.127.F1	0.025	3000	18333.3	6200	3846.2	1
48.0234	11	FPALNKMFCQL	1313	p53.127.F1	0.052	2482.8	5500	7750	500	2
48.0123	9	FPGTRVRAI	1314	p53.152.F1	1.1	-36000	662.7	23250	2439	1
48.0196	10	FPPGSTKRAL	1315	p53	0.79	-24000	6111.1	-23250	-20000	1
48.0127	9	FPQPKKKPI	1316	p53	0.61	-36000	-55000	-31000	16666.7	1
48.0128	9	FPQPKKKKPL	1317	p53	2.3	-36000	-55000	-31000	-100000	1

Table XXIII. Immunogenicity of A2 Supermotif Peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound	CTL Peptide <sup>1</sup>	CTL Wild-type	CTL Tumor
p53.135	9	CQLAKTCPV	1318	208	43.0	143.0	90.0	-- <sup>2</sup>	4		1/4	0/4
p53.69	8	AAPPVAPA	1319	5000	1536	1177	1233	4706	0			
p53.69L2V8	8	ALPPVAPV	1320	217	7167	500	285	67	4	2/4	1/3	0/3
p53.129	9	ALNKMFCQL	1321	735	391	19	73	-- <sup>2</sup>	3			
p53.129V9	9	ALNKMFCQV	1322	75	165	7.7	15	--	4	0/1		
p53.129B7V9	9	ALNKMFBQV	1323	192	391	23	49	--	4	2/4	0/3	0/2
p53.132	9	KMFCQLAKT	1324	333	33	18	106	--	4			
p53.132V9	9	KMFCQLAKV	1325	33	8.4	7.7	15	--	4	1/3	0/2	0/2
p53.132B4V9	9	KMFBQLAKV	1326	125	13	9.1	37	8889	4	5/5	0/4	0/4
p53.132L2V9	9	KLFCQLAKV	1327	98	3.6	3.4	9.5	1270	4	2/3	1/3	0/3
p53.139	9	KTCPVQLWV	1328	725	606	217	15	--	2			
p53.139L2	9	KLCPVQLWV	1329	122	239	29	23	--	4	2/5	2/3	1/3
p53.139L2B3	9	KLBPVQLWV	1330	45	29	19	31	--	4	3/4	2/3	1/2
p53.149	9	STPPPGTRV	1331	909	1162	1031	--	129	1			
p53.149L2	9	SLPPPGTRV	1332	122	226	13	9250	140	4	2/3	1/3	0/3
p53.149M2	9	SMPPPGTRV	1333	172	215	13	425	667	4	2/4	2/4	2/4
p53.216	10	VVVPYEPPEV	1334	617	1870	455	1194	--	1			
p53.216L2	10	VLVPYEPPEV	1335	89	391	71	2056	--	3	1/1	1/1	
p53.255	11	ITLEDSSGNLL	1336	1563	1265	2857	507	6667	0			
p53.255L2V11	11	ILLEDSSGNLV	1337	33	123	71	206	--	4	1/3	0/3	0/2

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity = 10,000nM.

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

A. Class I binding assays				Radiolabeled peptide		SEQ ID NO:
Species	Antigen	Allele	Cell line	Source	Sequence	
Human	A1	A*0101	Steinlin	Hu. J chain 102-110	YTAVVPLVY	1338
	A2	A*0201	JY	HBVc 18-27 F6->Y	FLPSDYFPSV	1339
	A2	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV	1340
	A2	A*0203		HBVc 18-27 F6->Y	FLPSDYFPSV	1341
	A2	A*0206	FUN	HBVc 18-27 F6->Y	FLPSDYFPSV	1342
	A2	A*0207	CLA	HBVc 18-27 F6->Y	FLPSDYFPSV	1343
	A2	A*0207	'21.221 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV	1344
	A3		GM3107	non-natural (A3CON1)	KVFPYALINK	1345
	A11		BVR	non-natural (A3CON1)	KVFPYALINK	1346
	A24	A*2402	KAS116	non-natural (A24CON1)	AYIDNYNKF	1347
	A31	A*3101	SPACH	non-natural (A3CON1)	KVFPYALINK	1348
	A33	A*3301	LWAGS	non-natural (A3CON1)	KVFPYALINK	1349
	A28/68	A*6801	CIR	HBVc 141-151 T7->Y	STLPETYVVR	1350
	A28/68	A*6802	AMAI	HBV pol 646-654 C4->A	FTQAGYPAL	1351
	B7	B*0702	GM3107	A2 sigal seq. 5-13 (L7->Y)	APRTL VYLL	1352
	B8	B*0801	Steinlin	IVgp 586-593 Y1->F, Q5->	FLKDYQLL	1353
	B27	B*2705	LG2	R 60s	FRYNGLIHR	1354
	B35	B*3501	C1R, BVR	non-natural (B35CON2)	FPFKYAAAF	1355
	B35	B*3502	TISI	non-natural (B35CON2)	FPFKYAAAF	1356
	B35	B*3503	EHM	non-natural (B35CON2)	FPFKYAAAF	1357
	B44	B*4403	PITOUT	EF-1 G6->Y	AEMGKYSFY	1358
	B51		KAS116	non-natural (B35CON2)	FPFKYAAAF	1359
	B53	B*5301	AMAI	non-natural (B35CON2)	FPFKYAAAF	1360
	B54	B*5401	KT3	non-natural (B35CON2)	FPFKYAAAF	1361
	Cw4	Cw*0401	C1R	non-natural (C4CON1)	QYDDAVYKL	1362
	Cw6	Cw*0602	721.221 transfected	non-natural (C6CON1)	YRHDGGNVL	1363
	Cw7	Cw*0702	721.221 transfected	non-natural (C6CON1)	YRHDGGNVL	1364
Mouse	D <sup>b</sup>		EL4	Adenovirus E1A P7->Y	SGPSNTYPEI	1365
	K <sup>b</sup>		EL4	VSV NP 52-59	RGYVFOGL	1366
	D <sup>d</sup>		P815	HIV-IIIIB ENV G4->Y	RGPYRAFTI	1367
	K <sup>d</sup>		P815	non-natural (KdCON1)	KFNPMKTYI	



Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

L <sup>d</sup>		P815	HBV <sub>s</sub> 28-39	IPQSLDSYWTSL	1368
B. Class II binding assays					
Species	Antigen	Allele	Cell line	Radiolabeled peptide	
				Source	Sequence
Human	DR1	DRB1*0101	LG2	HA Y307-319	YPKYVKQNTLKLAT
	DR2	DRB1*1501	L466.1	MBP 88-102Y	VVHFFKNIVTPRTPPY
	DR2	DRB1*1601	L242.5	non-natural (760.16)	YAAFAAAKTAATAFA
	DR3	DRB1*0301	MAT	MT 65kD Y3-13	YKTIADFEEARR
	DR4w4	DRB1*0401	Preiss	non-natural (717.01)	YARFQSQTTLKQKT
	DR4w10	DRB1*0402	YAR	non-natural (717.10)	YARFQRQTTLKAAA
	DR4w14	DRB1*0404	BIN 40	non-natural (717.01)	YARFQSQTTLKQKT
	DR4w15	DRB1*0405	KT3	non-natural (717.01)	YARFQSQTTLKQKT
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843	QYIKANSKFIGITE
	DR8	DRB1*0802	OLL	Tet. tox. 830-843	QYIKANSKFIGITE
	DR8	DRB1*0803	LUY	Tet. tox. 830-843	QYIKANSKFIGITE
	DR9	DRB1*0901	HID	Tet. tox. 830-843	QYIKANSKFIGITE
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	QYIKANSKFIGITE
	DR12	DRB1*1201	Herluf	unknown eluted peptide	EALHQLKINPYVLS
	DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A	QYIKANAKFIGITE
	DR51	DRB5*0101	GM3107 or L416.3	Tet. tox. 830-843	QYIKANAKFIGITE
	DR51	DRB5*0201	L255.1	HA 307-319	PKYVKQNTLKLAT
	DR52	DRB3*0101	MAT	Tet. tox. 830-843	NGQIGNDPNRDIL
	DR53	DRB4*0101	L257.6	non-natural (717.01)	YARFQSQTTLKQKT
	DQ3.1	DQA1*0301/DQB1*030	PF	non-natural (ROIV)	YAHAAHAAHAAHAAHAA
Mouse	IA <sup>b</sup>		DB27.4	non-natural (ROIV)	YAHAAHAAHAAHAAHAA
	IA <sup>d</sup>		A20	non-natural (ROIV)	YAHAAHAAHAAHAAHAA
	IA <sup>k</sup>		CH-12	HEL 46-61	YNTDGSITDYGILQINSR
	IA <sup>s</sup>		LS102.9	non-natural (ROIV)	YAHAAHAAHAAHAAHAA
	IA <sup>u</sup>		91.7	non-natural (ROIV)	YAHAAHAAHAAHAAHAA
	IE <sup>d</sup>		A20	Lambda repressor 12-26	YLEDARRKKAIYEKKK
	IE <sup>k</sup>		CH-12	Lambda repressor 12-26	YLEDARRKKAIYEKKK

all  
conclude

**Table XXVI. Crossbinding of A2 supermotif peptides**

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound
p53.24	9	KLLPENNVVL	1396	313	1955	--	1194	--	1
p53.25	11	LLPENNVLSPL	1397	19	6.2	4.5	12	1702	4
p53.65	10	RMPEAAPVA	1398	78	102	13	841	--	3
p53.65	9	RMPEAAPV	1399	119	23	22	70	--	4
p53.113	10	FLHSGTAKSV	1400	357	179	15	4625	--	3
p53.132	9	KMFCQLAKT	1401	333	33	18	106	--	4
p53.135	9	CQLAKTCPV	1402	208	43	143	90	--	4
p53.136	8	QLAKTCPV	1403	455	--	100	2643	1067	2
p53.164	9	KQSQHMTEV	1404	500	130	170	285	--	4
p53.187	11	GLAPPQHLIRV	1405	79	39	11	55	--	4
p53.193	11	HLIRVEGNLRV	1406	385	1387	83	1194	1778	2
p53.229	9	CTTIHYNM	1407	278	287	2564	561	181	3
p53.263	10	NLLGRNSFEV	1408	217	--	2500	881	--	1
p53.264	9	LLGRNSFEV	1409	85	358	37	206	--	4

-- indicates binding affinity = 10,000nM.

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Comp.

Table XXVII. Immunogenicity of A2 supermotif peptides

Source	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound	CTL Wild-type <sup>1</sup>	CTL Tumor
p53.135	CQLAKTCPV	1410	208	43	143	90	-- <sup>2</sup>	4	1/4	0/1

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity = 10,000nM.

**Table XXVIII. Crossbinding of A2 supermotif analogs**

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound
p53.69	8	AAPPVAPA	1411	5000	1536	1177	1233	4706	0
p53.69L2V8	8	ALPPVAPV	1412	217	7167	500	285	67	4
p53.101	11	KTYQGSYGRL	1413	1786	896	--	514	615	0
p53.101L2V1	11	KLYQGSYGFRV	1414	81	48	24	116	--	4
p53.129	9	ALNKMFCQL	1415	735	391	19	73	--	3
p53.129V9	9	ALNKMFCQV	1416	75	165	7.7	15	--	4
p53.129B7V9	9	ALNKMFBQV	1417	192	391	23	49	--	4
p53.129	10	ALNKMFCQLA	1418	1316	1075	71	4625	--	1
p53.129V10	10	ALNKMFCQLV	1419	217	287	71	7400	--	3
p53.132	9	KMFCQLAKT	1420	333	33	18	106	--	4
p53.132V9	9	KMFCQLAKV	1421	33	8.4	7.7	15	--	4
p53.132B4V9	9	KMFBQLAKV	1422	125	13	9.1	37	8889	4
p53.132L2V9	9	KLFCQLAKV	1423	98	3.6	3.4	10	1270	4
p53.135	9	QLAKTCPV	1424	208	43	143	90	--	4
p53.135L2	9	CLLAKTCPV	1425	125	506	67	370	--	3
p53.135B1B7	9	BQLAKTBPV	1426	102	71	15	67	--	4
p53.135B1L2I	9	BLLAKTBPV	1427	46	119	7.7	64	--	4
p53.139	9	KTCPVQLWV	1428	725	606	217	15	--	2
p53.139L2	9	KLCPVQLWV	1429	122	239	29	23	--	4
p53.139L2B3	9	KLBPVQLWV	1430	46	29	19	31	--	4
p53.149	9	STPPPGTRV	1431	909	1162	1031	--	129	1
p53.149M2	9	SMPPPGTRV	1432	172	215	13	425	667	4
p53.149L2	9	SLPPPGTRV	1433	122	226	13	9250	140	4
p53.164	9	KSQHMTVEV	1434	500	130	170	285	--	4
p53.164L2	9	KLQHMTVEV	1435	122	94	35	46	--	4
p53.216	10	VVVPYEPPEV	1436	617	1870	455	1194	--	1
p53.216L2	10	VLVPYEPPEV	1437	89	391	71	2056	--	3
p53.236	11	YMCNSSCMGGM	1438	667	391	67	974	5333	2
p53.236L2M1	11	YLCNSSCMGGV	1439	22	13	3.6	18	1569	4
p53.255	11	ITLEDSSGNLL	1440	1563	1265	2857	507	6667	0
p53.255L2V1	11	ILLEDSSGNLV	1441	33	123	71	206	--	4

-- indicates binding affinity = 10,000nM.

Table XXIX. Immunogenicity of A2 supermotif analogs

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound	CTL Peptide <sup>1</sup>	CTL Wild-type	CTL Tumor
p53.69	8	AAPPVAPA	1442	5000	1536	1177	1233	4706	0			
p53.69L2V8	8	ALPPVAPV	1443	217	7167	500	285	67	4	2/4	1/3	0/3
p53.129	9	ALNKMFCQL	1444	735	391	19	73	-- <sup>2</sup>	3			
p53.129V9	9	ALNKMFCQV	1445	75	165	7.7	15	--	4	0/1		
p53.129B7V9	9	ALNKMFBQV	1446	192	391	23	49	--	4	2/4	0/3	0/2
p53.132	9	KMFCQLAKT	1447	333	33	18	106	--	4			
p53.132V9	9	KMFCQLAKV	1448	33	8.4	7.7	15	--	4	1/3	0/2	0/2
p53.132B4V9	9	KMFBQLAKV	1449	125	13	9.1	37	8889	4	5/5	0/4	0/4
p53.132L2V9	9	KLFCQLAKV	1450	98	3.6	3.4	9.5	1270	4	2/3	1/3	0/3
p53.139	9	KTCPVQLWV	1451	725	606	217	15	--	2			
p53.139L2	9	KLCPVQLWV	1452	122	239	29	23	--	4	2/5	2/3	1/3
p53.139L2B3	9	KLBPVQLWV	1453	45	29	19	31	--	4	3/4	2/3	1/2
p53.149	9	STPPGTRV	1454	909	1162	1031	--	129	1			
p53.149L2	9	SLPPGTRV	1455	122	226	13	9250	140	4	2/3	1/3	0/3
p53.149M2	9	SMPPPGTRV	1456	172	215	13	425	667	4	2/4	2/4	2/4
p53.216	10	VVVPYEPPEV	1457	617	1870	455	1194	--	1			
p53.216L2	10	VLVPYEPPEV	1458	89	391	71	2056	--	3	1/1	1/1	
p53.255	11	ITLEDSSGNLL	1459	1563	1265	2857	507	6667	0			
p53.255L2V11	11	ILLEDSSGNLV	1460	33	123	71	206	--	4	1/3	0/3	0/2

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity = 10,000nM.

**Table XXX. DR supertype primary binding**

A7  
Cont.

Peptide	DR147 Algo Sum	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR147 Cross- binding
39.0307	2	GFRLGFLHSGTAKSV	1461	P53.108	3	5.4	89	3
39.0308	2	LNKMFCQLAKTCPVQ	1462	P53.130	20	804	167	3
39.0309	2	MGGMNRRPILTIITL	1463	P53.243	--	--	--	0
39.0310	2	RRPILTIITLEDSSG	1464	P53.248	5000	4500	--	0
39.0311	2	KRALPNNTSSSPQPK	1465	P53.305	--	--	--	0
39.0312	2	DGEYFTLQIRGRERF	1466	P53.324	125	--	--	1

-- indicates binding affinity =10,000nM.

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Conf.

Table XXXI. DR supertype cross-binding

Peptide	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR2w2 $\beta$ 1 nM	DR2w2 $\beta$ 2 nM	DR6w1 9 nM	DR5w1 1 nM	DR8w2 nM	DR147 Binding	Broad Binding (5/8)
39.0307	GFRLGFLHSGTAKSV	1467	p53.108	2.6	5.4	89	253	167	76	100	29	3	8
39.0308	LNKMFCQLAKTCPV	1468	p53.130	20	804	167	5688	541	365	2500	1531	3	5

-- indicates binding affinity = 10,000nM.

Table XXXII. DR3 binding

Peptide	Sequence	SEQ ID NC	Source	DR3 nM
39.0409	EPPLSQETFSDLWKL	1469	p53.11	--
39.0410	LWKLLPENNVLSPLP	1470	p53.22	--
39.0411	DLMLSPDDIEQWFTE	1471	p53.42	--
39.0412	EQWFTEDPGPDEAPR	1472	p53.51	--
39.0413	PVQLWVDSTPPPGTR	1473	p53.142	--
39.0414	MAIYKQSQHMTEVVR	1474	p53.160	--
39.0415	QHLIRVEGNLRVEYL	1475	p53.192	3125
39.0416	LIRVEGNLRVEYLDD	1476	p53.194	3226
39.0417	EGNLRVEYLDDRNTF	1477	p53.198	--
39.0418	RVEYLDDRNTFRHSV	1478	p53.202	1667
39.0419	SVVVPYEPPEVGSDC	1479	p53.215	--
39.0420	PPEVGSDCTTIHYN	1480	p53.222	7895
39.0421	LTIITLEDSSGNLLG	1481	p53.252	--
39.0422	KKPLDGEYFTLQIRG	1482	p53.320	--
39.0423	GEYFTLQIRGRERFE	1483	p53.325	--
39.0424	RFEMFRELNEALELK	1484	p53.337	--

-- indicates binding affinity =10,000nM.

Q17  
Conf.



Table XXXIII. HTL candidate peptides

*Q7 conclude*

Peptide	Sequence	SEQ ID NO:	DR1 nM	DR4w nM	DR7 nM	DR3 nM	DR2w 2 $\beta$ 1 nM	DR2w 2 $\beta$ 2 nM	DR6w 9 nM	DR5w 1 nM	DR8w 2 nM	DR14 7 Bindin g	Broad Binding (5/8)	DR 3 Binder
39.0307	GFRLGFLHSGTAKSV	1485p53.108	2.6	5.4	89	--	253	167	76	100	29	3	8	0
39.0308	LNKMFCQLAKTCPVQ	1486p53.130	20	804	167	--	5688	541	365	2500	1531	3	5	0

-- indicates binding affinity = 10,000nM.

column added

Table IV. HLA Class I Standard Peptide Binding Affinity.

ALLELE	STANDARD PEPTIDE	SEQUENCE	SEQ ID NO:	STANDARD BINDING AFFINITY (nM)
A*0101	944.02	YLEPAIAKY	1189	25
A*0201	941.01	FLPSDYFPSV	1190	5.0
A*0202	941.01	FLPSDYFPSV	1191	4.3
A*0203	941.01	FLPSDYFPSV	1192	10
A*0205	941.01	FLPSDYFPSV	1193	4.3
A*0206	941.01	FLPSDYFPSV	1194	3.7
A*0207	941.01	FLPSDYFPSV	1195	23
A*6802	1072.34	YVIKVSARV	1196	8.0
A*0301	941.12	KVFPYALINK	1197	11
A*1101	940.06	AVDLYHFLK	1198	6.0
A*3101	941.12	KVFPYALINK	1199	18
A*3301	1083.02	STLPETYVVRR	1200	29
A*6801	941.12	KVFPYALINK	1201	8.0
A*2402	979.02	AYIDNYNKF	1202	12
B*0702	1075.23	APRTLVLVLL	1203	5.5
B*3501	1021.05	FPFKYAAAF	1204	7.2
B51	1021.05	FPFKYAAAF	1205	5.5
B*5301	1021.05	FPFKYAAAF	1206	9.3
B*5401	1021.05	FPFKYAAAF	1207	10

Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	Sequence	SEQ ID NO:	Binding Affinity (nM)
DRB1*0101	DR1	515.01	PKYVKQNTLKLAT	1208	5.0
DRB1*0301	DR3	829.02	YKTIAFDEEARR	1209	300
DRB1*0401	DR4w4	515.01	PKYVKQNTLKLAT	1210	45
DRB1*0404	DR4w14	717.01	YARFQSQTTLKQKT	1211	50
DRB1*0405	DR4w15	717.01	YARFQSQTTLKQKT	1212	38
DRB1*0701	DR7	553.01	QYIKANSKFIGITE	1213	25
DRB1*0802	DR8w2	553.01	QYIKANSKFIGITE	1214	49
DRB1*0803	DR8w3	553.01	QYIKANSKFIGITE	1215	1600
DRB1*0901	DR9	553.01	QYIKANSKFIGITE	1216	75
DRB1*1101	DR5w11	553.01	QYIKANSKFIGITE	1217	20
DRB1*1201	DR5w12	1200.05	EALIHQLKINPYVLS	1218	298
DRB1*1302	DR6w19	650.22	QYIKANAKFIGITE	1219	3.5
DRB1*1501	DR2w2 $\beta$ 1	507.02	GRTQDENPVVHFFKNIVTP RTPPP	1220	9.1
DRB3*0101	DR52a	511	NGQIGNDPNRDIL	1221	470
DRB4*0101	DRw53	717.01	YARFQSQTTLKQKT	1222	58
DRB5*0101	DR2w2 $\beta$ 2	553.01	QYIKANSKFIGITE	1223	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

Return moved from  
covid panel

Table XIX  
p53 DR Super Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w01	DR2w02	DR3	DR4w4	DR4w15	DR5w11	DR5w12
VTCTSPAL	1123	AKSVTCYSPALNKM	1057	119								
LKDAQAGKE	1124	ALELKDAQAGKEPGG	1058	347								
VAPAPAPT	1125	APPVAPAPAPTAA	1059	70								
MPEAAPVA	1126	APRMPEAAPVAPAP	1060	63								
WPLSSSVPS	1127	APSWPLSSSVPSQKT	1061	88								
IHYNYMCS	1128	CTTIHYNYMCSNCSM	1062	229								
YFTLIQGR	1129	DGEYFTLIQGRERF	1063	324				-0.0027				
LSPDDIEQW	1130	DLMLSPDDIEQWTFE	1064	42	0.0400			0.0150				
VEPPLSQET	1131	DPSVEPPLSQETFS	1065	7				0.0039				
LRVEYDDR	1132	EGNLRVEYDDRNTF	1066	198								
VLSPLPSQA	1133	ENNVLSPLPSQAMDD	1067	28								
LAKTCPVQL	1134	FCQLAKTCPVQLWVD	1068	134								
LWKLPPENN	1135	FSDLWKLPPENNVL	1069	19								
LGFLHSGTA	1136	GFLRGLHSGTAKSV	1070	108								
VRAMAIYKQ	1137	GTRVRAMAIYKQSQH	1071	154	1.9000	0.0360	0.1200	0.0027	8.3000		0.2000	
LPGSTKRA	1138	HHELPGSTKRALPN	1072	296								
VVPYEPPEV	1139	HSVVVPYEPPEVGS	1073	214								
YMCNSSCMG	1140	HYNYMCSNCSMGGMN	1074	233								
WFTEDPGPD	1141	IEQWFTEDPGDEAP	1075	50								
LPNTSSSP	1142	KRALPNNTSSSPQPK	1076	305	-0.0005				-0.0027			
LHSGTAKSV	1143	LGFLHSGTAKSVTCT	1077	111								
MFCQLAKTC	1144	LNMFCQLAKTCPVQ	1078	130	0.2500	0.0016	0.0370	0.0006	0.0560		0.0080	
LFSQAMDDL	1145	LSPLFSQAMDDLMLS	1079	32				0.0030				
ITLEDSSGN	1146	LTIITLEDSSGNLLG	1080	252	-0.0005				-0.0027			
MNRRLPITI	1147	MGMNRRLPITIITL	1081	243								
VVRCPHIE	1148	MTEVVRCPHIEHRS	1082	169								
LELKDAQAG	1149	NEALELKDAQAGKEP	1083	345								
LSPLPSQAM	1150	NNVLSPLPSQAMDDL	1084	29								
IEQWFTEDP	1151	PDEIQWFTEDPGPD	1085	47								
VGSDCTTIH	1152	PPEVGSCTTIHNY	1086	222								
LWVDSTPPP	1153	PVQLWVDSTPPPGR	1087	142				0.0380				
VDSTPPPGT	1154	QLWVDSTPPPGTRVR	1088	144				0.0300				
FLHSGTAKS	1155	RLGFLHSGTAKSVTC	1089	110								
FEVRVCACP	1156	RNSFEVRVCACPGRD	1090	267								
FRHSVVVPY	1157	RNFRHSVVVPYEP	1091	209								
LTIITLED	1158	RPILTITLEDSSGN	1092	249								
VRVCACPGR	1159	RRPILTITLEDSSG	1093	248	0.0010				0.0100			
LLGRNSFEV	1160	SFEVRVCACPGRDR	1094	269								
LNMFCQLA	1161	SGNLLGRNSFEVRVC	1095	261								
MDDLMLSPD	1162	SPALNLMFCQLAKTC	1096	127								
VPSQKTYQG	1163	SOAMDMLMLSPDDIE	1097	37								
VPYEPPEVG	1164	SSSVPSQKTYQGSYG	1098	94								
LSSSVPSQK	1165	SVVVPYEPPEVGSDC	1099	215								
FRLGFLHSG	1166	SWPLSSSVPSQKTYQ	1100	90				-0.0025				
LDRNTRFH	1167	SYGFLGFLHSGTAK	1101	106								
WVDSTPPPG	1168	VEYLDNRNTRHRSV	1102	203								
YEPPEVGS	1169	VQLWVDSTPPPGTRV	1103	143								
LPENNVLSP	1170	VVPYEPPEVGSCTTI	1104	217								
MCNSSCMGG	1171	WKLLPENNVLSP	1105	23								
	1172	YNYMCSNCSMGGMNR	1106	234								

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Table XIX  
p53 DR Super Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
VTCTYSPAL	1123	AKSVTCTYSPALNKM	1057					
LKDAQAGKE	1124	ALELKDAQAGKEPGG	1058					
VAPAPAPT	1125	APPVAPAPAPTAA	1059					
MPEAAPVA	1126	APRMPEAAPVAPAP	1060					
WPLSSVPS	1127	APSWPLSSVPSQKT	1061					
IHYNYMCNS	1128	CTTIHYNYMCNSSCM	1062					
YFTLQIRGR	1129	DGEYFTLQIRGRERF	1063					
LSPDDIEQW	1130	DLMLSPDDIEQWTFE	1064		-0.0018			
VEPPLSQET	1131	DPSVEPPLSQETFS	1065					
LRVEYLDNR	1132	EGNLRVEYLDNRNIF	1066					
VLSPLPSQA	1133	ENNVLSPLPSQAMDD	1067					
LAKTCPVQL	1134	FCQLAKTCPVQLWVD	1068					
LWKLPPENN	1135	FSDLWKLPPENNVL	1069					
GFLHSGTA	1136	GFLHSGTAQSV	1070	0.0460	0.2800	1.7000		
VRAMAIYKQ	1137	GTRVAMAIYKQSOH	1071					
LPFGSTKRA	1138	HHELPGSTKRALPN	1072					
VVPYEPPEV	1139	HSVVVPYEPPEVGS	1073					
YMCNSSCMG	1140	HYNYMCNSSCMGGMN	1074					
WFTEDPGPD	1141	IEQWFTEDPGDEAP	1075		-0.0007			
LPNNTSSSP	1142	KRALPNNTSSSPQPK	1076					
LHSGTAKSV	1143	LGFLHSGTAKSVTCT	1077					
MFQOLAKTC	1144	LNMFCQOLAKTCPVQ	1078	0.0096	0.1500	0.0320		
LPSQAMDDL	1145	LSPLSQAMDDLMLS	1079					
LTLEDSSGN	1146	LTLEDSSGNLLG	1080		-0.0007			
MNRRLPITI	1147	MGMNRRRLPITIIL	1081					
VVRCPHIE	1148	MTEVVRCPHIERCS	1082					
LELKDAQAG	1149	NEALELKDAQAGKEP	1083					
LSPLPSQAM	1150	NNVLSPLPSQAMDDL	1084					
IEQWFTEDP	1151	PDDIEQWFTEDPGPD	1085					
VGSDCTIHH	1152	PEVGSCTIHHYNY	1086					
LWVDSTPPP	1153	PVQLWVDSTPPPGTR	1087					
VDSSTPPGT	1154	QLWVDSTPPPGTRVR	1088					
FLHSGTAKS	1155	RLGFLHSGTAKSVTC	1089					
FEVRVCACP	1156	RNSFEVRVCACPGRD	1090					
FRHSVVVPY	1157	RNTERHSVVVPYEP	1091					
LTITLEDSD	1158	RPILTIITLEDSSGN	1092					
ILTIITLED	1159	RRPILTIITLEDSSG	1093		0.0023			
VRVCACPGR	1160	SFEVRVCACPGDRDR	1094					
LLGRNSFEV	1161	SGNLLGRNSFEVRVC	1095					
LNMFCQLA	1162	SPALNLMFCQLAKTC	1096					
MDDLMLSPD	1163	SOAMDDLMLSPDDIE	1097					
VPSQKTYQG	1164	SSSVPSQKTYQGSYG	1098					
VYVEPPEVG	1165	SVVVPYEPPEVGSDC	1099					
LSSSVPSQK	1166	SWPLSSSVPSQKTYQ	1100					
FRGLFLHSG	1167	SYGFRGLFLHSGTAK	1101					
LDRNTERH	1168	VEYLDNRNTERHSVV	1102					
WVDSTPPPG	1169	VQLWVDSTPPPGTRV	1103					
YEPPEVGS	1170	VVPYEPPEVGSDCIT	1104					
LPENNVLSP	1171	WKLLPENNVLSPLS	1105					
MCNSSCMGG	1172	YNYMCNSSCMGGMNR	1106					

Table XXa p53 DR 3a Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w2B1	DR2w2B2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LSPDDIEQW	1173	DLMLSPDDIEQWFTE	1107	42				0.0150				
LRVEYLLDR	1174	EGNLRVEYLLDRNTF	1108	198				0.0039				
LSQETESDL	1175	EPPLSQETESDLWKL	1109	11				-0.0025				
FTEDPGFDE	1176	EQWFTEDPGPDEAPR	1110	51				-0.0025				
LDGEYFTLQ	1177	KKPLDGEYFTLQIRG	1111	320				-0.0025				
ITLEDSSGN	1178	LTITLEDSSGNLLG	1112	252				0.0030				
LLPENNVL	1179	LWKLLPENNVLSPLP	1113	22				0.0029				
VGSDCTTH	1180	PPEVGSDCCTTHYNY	1114	222				0.0380				
LWVDSTPPP	1181	PVQLWVDSTPPPQTR	1115	142				0.0300				
IRVEGNLRV	1182	QHLIRVEGNLRVEYL	1116	192				0.0960				
MFRELNEAL	1183	RFEMFRELNEALELK	1117	337				0.0052				
YLLDRNTFR	1184	RVEYLLDRNTFRHSV	1118	202				0.1800				
VPYEPPEVG	1185	SVVVPYEPPEVGSDC	1119	215				-0.0025				

p53-DR-3a Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LSPDDIEOW	1173	DLMLSPDDIEQWFTF	1107					
LRVEYLDNR	1174	EGNLRVEYLDNRNTF	1108					
LSQETESDL	1175	EPPLSQETESDLWKL	1109					
FTEDPGFDE	1176	EQWFTEDPGDEAPR	1110					
LDGEYFTLO	1177	KKPLDGEYFTLQIRG	1111					
ITLEDSSGN	1178	LITILEDSSGNLLG	1112					
LLPENNVL	1179	LWKLLPENNVLPLP	1113					
VGSDCTTH	1180	PPEVGSDCTTHYNY	1114					
LWVDSTPP	1181	PVQLWVDSTPPGTR	1115					
IRVEGNLRV	1182	QHLIRVEGNLRVEYL	1116					
MFRELNEAL	1183	RFEMFRELNEALELK	1117					
YLDNRNTR	1184	RVEYLDNRNTRHSV	1118					
VPYEPPEVG	1185	SVVVPYEPPEVGSDC	1119					

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monoclonal  
antibodies

Table XXb p53 DR 3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w201	DR2w282	DR3	DR4w4	DR4w15	DR5w11	DR5w12
FTLQIRGRE	1186	GEYFTLQIRGRERFE	1120	325				0.0290				
VEGNLRVEY	1187	LIRVEGNLRVEYLLDD	1121	194				0.0930				
YKQSQHMTTE	1188	MAIYKQSQHMTTEVVR	1122	160				-0.0025				

Handwritten notes and arrows pointing to the table data.



Table XXb p53 DR 3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
FTLQIRGRE	1186	GEYFTLQIRGRERFE	1120					
VEGNLRVEY	1187	LIRVEGNLRVEYLLDD	1121					
YKQSQHMT	1188	MAIKQSQSQHMTTEVVR	1122					

*[Handwritten signature]*

*[Handwritten notes: "DR 3b", "p53", "DR 3b"]*

*[Handwritten notes: "FTLQIRGRE", "VEGNLRVEY", "YKQSQHMT"]*

Table XXII. A2 supermotif analogs

Source	AA	Sequence	SEQ ID NO:	A*0201 nM
p53.24	9	KLLPENNVVL	1224	313
p53.24V9	9	KLLPENNVV	1225	385
p53.25	11	LLPENNVLSPL	1226	19
p53.25V9	11	LLPENNVLSPV	1227	39
p53.65	9	RMPEAAPPV	1228	119
p53.65L2	9	RLPEAAPPV	1229	78
p53.65	10	RMPEAAPVA	1230	78
p53.65L2V10	10	RLPEAAPVV	1231	143
p53.65M2V10	10	RMPEAAPVV	1232	54
p53.69	8	AAPPVAPA	1233	5000
p53.69L2V8	8	ALPPVAPV	1234	217
p53.101	11	KTYQGSYGFR	1235	1786
p53.101L2V11	11	KLYQGSYGFRV	1236	81
p53.113	11	FLHSGTAKSVT	1237	5000
p53.113V11	11	FLHSGTAKSVV	1238	1220
p53.129	9	ALNKMFCQL	1239	735
p53.129V9	9	ALNKMFCQV	1240	75
p53.129B7V9	9	ALNKMFBQV	1241	192
p53.129	10	ALNKMFCQLA	1242	1316
p53.129V10	10	ALNKMFCQLV	1243	217
p53.132	9	KMFCQLAKT	1244	333
p53.132V9	9	KMFCQLAKV	1245	33
p53.132B4V9	9	KMFBQLAKV	1246	125
p53.132L2V9	9	KLFCQLAKV	1247	98
p53.135	9	CQLAKTCPV	1248	208
p53.135L2	9	CLLAKTCPV	1249	125
p53.135B1B7	9	BQLAKTBPV	1250	102
p53.135B1L2B7	9	BLLAKTBPV	1251	46
p53.139	9	KTCPVQLWV	1252	725
p53.139L2	9	KLCPVQLWV	1253	122
p53.139L2B3	9	KLBPVQLWV	1254	46
p53.149	9	STPPPGTRV	1255	909
p53.149M2	9	SMPPPGTRV	1256	172
p53.149L2	9	SLPPPGTRV	1257	122
p53.164	9	KQSQHMTEV	1258	500
p53.164L2	9	KLSQHMTEV	1259	122
p53.216	10	VVVPYEPPEV	1260	617
p53.216L2	10	VLVPYEPPEV	1261	89
p53.229	9	CTTIHYNM	1262	278
p53.229L2V9	9	CLTIHYNV	1263	263
p53.229B1L2V9	9	BLTIHYNV	1264	116
p53.236	8	YMCNSSCM	1265	4546
p53.236L2M8	8	YLCNSSCV	1266	-
p53.236	11	YMCNSSCMGGM	1267	667
p53.236L2M11	11	YLCNSSCMGGV	1268	22
p53.255	11	ITLEDSSGNLL	1269	1563
p53.255L2V11	11	ILLEDSSGNLV	1270	33
p53.256	10	TLEDSSGNLL	1271	1667
p53.256V10	10	TLEDSSGNLV	1272	4167

Table XXIIA A01 Analog Peptides

<u>Peptide</u>	<u>AA</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>A*0101 nM</u>
52.0136	11	GSDCTTIHYN	1273	p53.226	67.6
57.0035	9	GTDCTTIHY	1274	p53.226.T2	0.9
57.0125	10	PTQKTYQGSY	1275	p53.98.T2	35.7
57.0126	10	GTDKSVTCTY	1276	p53.117.D3	42.4
57.0127	10	RVDGNLRVEY	1277	p53.196.D3	45.5

Table XXIIIB A03 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	A*0301 nM	A*1101 nM	A*3101 nM	A*3301 nM	A*6801 nM	A3 XRN
1371.14	10	KVYQGSYGFR	1278	p53.101.V2	37.9	61.9	72	10000	40	4
1371.15	10	KVYQGSYGFK	1279	p53.101.V2K10	33.3	9.2	138.5	-72500	38.1	4
1371.16	9	BVYSPALNK	1280	p53.124.B1V2	15.7	12.8	439	22307.7	500	4
1371.17	9	BVYSPALNR	1281	p53.124.B1V2R9	25	8.3	33.3	85.3	14.8	5
1371.18	8	KVFBQLAK	1282	p53.132.V2B4	846.2	461.5	7500	-72500	8888.9	1
1371.2	11	GVRVRAMAIYK	1283	p53.154.V2	57.9	136.4	418.6	-72500	13333.3	3
1371.22	9	RVRAMAIYR	1284	p53.156.R9	40.7	1666.7	8.6	138.1	666.7	3
1371.24	9	SVBMGGMNK	1285	p53.240.V2B3K9	12.5	17.1	9000	-72500	29.6	3
1371.25	10	SVBMGGMNRK	1286	p53.240.V2B3K10	100	75	-36000	-72500	17	3
1371.26	9	SVBMGGMNR	1287	p53.240.V2B3	161.8	95.2	120	852.9	11.1	4
1371.27	10	SVBMGGMNR	1288	p53.240.V2B3	1000	25	620.7	805.6	11.4	2
1371.31	11	RVBABPGDRDK	1289	p53.273.B3B5K11	314.3	200	4615.4	-72500	2500	2
1371.32	11	SVSRHKKLMFK	1290	p53.376.V2	33.3	54.5	295.1	18125	1509.4	3
1371.33	11	SVSRHKKLMFR	1291	p53.376.V2R11	196.4	2857.1	183.7	1381	500	3

added  
p53.101.V2

Table XXII C A02 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	A2 XRN
27.0068	9	KMFCQLAKT	1292	p53.132	505.1	14.3	19.6	92.5	-40000	3
39.0074	9	LLGRDSFEV	1293	mp53.261	41.7					
44.0003	9	LLGRDSFEV	1294	mp53.261	27.8					
1317.22	9	ALNKMFCQL	1295	p53.129	735.3	390.9	18.5	72.5	-80000	3
1317.23	9	KMFCQLAKT	1296	p53.132	333.3	33.1	17.5	105.7	-80000	4
1324.08	9	KQSQHMTEV	1297	p53.164	500	130.3	169.5	284.6	-80000	4
1329.04	9	CTTIHNYM	1298	p53.229	277.8	286.7	2564.1	560.6	181.8	3
1329.07	9	KLLPENNVL	1299	p53.24	312.5	1954.5	12500	1193.5	-80000	1
1329.09	10	FLHSGTAKSV	1300	p53.113	357.1	179.2	14.5	4625	80000	3

added  
column

Table XXIID A24 Analog Peptides

<u>Peptide</u>	<u>AA</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>A*2401 nM</u>
52.008	8	TYQGSYGF	1301	p53.102	109.1
52.0081	8	SYGFRLGF	1302	p53.106	428.6
52.0103	10	TYQGSYGFRL	1303	p53.102	100
52.0104	10	TYSPALNKMF	1304	p53.125	2.4
52.0144	11	TYLWWVNNQSL	1305	CEA.353	46.2
52.0147	11	TYLWWVNGQSL	1306	CEA.531	92.3
57.0042	9	LYWVNGQSF	1307	CEA.533.Y2F9	15.8
57.0051	9	EYVNARHCF	1308	Her2/neu.553.F9	150
57.007	9	TYSDLWKLF	1309	p53.18.Y2F9	5.5
57.0071	9	SYGFRLGFF	1310	p53.106.F9	121.2
57.0096	10	TYQGSYGFRR	1311	p53.102.F10	30

TABLE XXIIIE B07 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	B*0702 nM	B*3501 nM	B*5101 nM	B*5301 nM	B*5401 nM	B7 XRN
48.0055	8	FPALNKMIF	1312	p53.127.F1	0.025	3000	18333.3	6200	3846.2	1
48.0234	11	FPALNKMFCQL	1313	p53.127.F1	0.052	2482.8	5500	7750	500	2
48.0123	9	FPGTRVRAI	1314	p53.152.F1	1.1	-36000	662.7	23250	2439	1
48.0196	10	FPPGSTKRAL	1315	p53	0.79	-24000	6111.1	-23250	-20000	1
48.0127	9	FPQPKKKPI	1316	p53	0.61	-36000	-55000	-31000	16666.7	1
48.0128	9	FPQPKKKPL	1317	p53	2.3	-36000	-55000	-31000	-100000	1

added column

Table XXIII. Immunogenicity of A2 Supermotif Peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound	CTL Peptide <sup>1</sup>	CTL Wild-type	CTL Tumor
p53.135	9	QQLAKTCPV	1318	208	43.0	143.0	90.0	-- <sup>2</sup>	4		1/4	0/4
p53.69	8	AAPPVAPA	1319	5000	1536	1177	1233	4706	0			
p53.69L2V8	8	ALPPVAPV	1320	217	7167	500	285	67	4	2/4	1/3	0/3
p53.129	9	ALNKMFCQL	1321	735	391	19	73	-- <sup>2</sup>	3			
p53.129V9	9	ALNKMFCQV	1322	75	165	7.7	15	--	4	0/1		
p53.129B7V9	9	ALNKMFBQV	1323	192	391	23	49	--	4	2/4	0/3	0/2
p53.132	9	KMFCQLAKT	1324	333	33	18	106	--	4			
p53.132V9	9	KMFCQLAKV	1325	33	8.4	7.7	15	--	4	1/3	0/2	0/2
p53.132B4V9	9	KMFBQLAKV	1326	125	13	9.1	37	8889	4	5/5	0/4	0/4
p53.132L2V9	9	KLFCQLAKV	1327	98	3.6	3.4	9.5	1270	4	2/3	1/3	0/3
p53.139	9	KTCPVQLWV	1328	725	606	217	15	--	2			
p53.139L2	9	KLCPVQLWV	1329	122	239	29	23	--	4	2/5	2/3	1/3
p53.139L2B3	9	KLBPVQLWV	1330	45	29	19	31	--	4	3/4	2/3	1/2
p53.149	9	STPPPGTRV	1331	909	1162	1031	--	129	1			
p53.149L2	9	SLPPPGTRV	1332	122	226	13	9250	140	4	2/3	1/3	0/3
p53.149M2	9	SMPPPGTRV	1333	172	215	13	425	667	4	2/4	2/4	2/4
p53.216	10	VVVPYEPPEV	1334	617	1870	455	1194	--	1			
p53.216L2	10	VLVPYEPPEV	1335	89	391	71	2056	--	3	1/1	1/1	
p53.255	11	ITLEDSSGNLL	1336	1563	1265	2857	507	6667	0			
p53.255L2V11	11	ILEDDSSGNLV	1337	33	123	71	206	--	4	1/3	0/3	0/2

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity = 10,000nM.

*Handwritten:* 8002000

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Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

A. Class I binding assays				Radiolabeled peptide		SEQ ID NO:
Species	Antigen	Allele	Cell line	Source	Sequence	
Human	A1	A*0101	Steinlin	Hu. J chain 102-110	YTAVVPLVY	1338
	A2	A*0201	JY	HBVc 18-27 F6->Y	FLPSDYFPSV	1339
	A2	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV	1340
	A2	A*0203	FUN	HBVc 18-27 F6->Y	FLPSDYFPSV	1341
	A2	A*0206	CLA	HBVc 18-27 F6->Y	FLPSDYFPSV	1342
	A2	A*0207	'21.221 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV	1343
	A3		GM3107	non-natural (A3CON1)	KVFPYALINK	1344
	A11		BVR	non-natural (A3CON1)	KVFPYALINK	1345
	A24	A*2402	KAS116	non-natural (A24CON1)	AYIDNVNKF	1346
	A31	A*3101	SPACH	non-natural (A3CON1)	KVFPYALINK	1347
	A33	A*3301	LWAGS	non-natural (A3CON1)	KVFPYALINK	1348
	A28/68	A*6801	C1R	HBVc 141-151 T7->Y	STLPETYVVR	1349
	A28/68	A*6802	AMAI	HBV pol 646-654 C4->A	FTQAGYPAL	1350
	B7	B*0702	GM3107	A2 sigal seq. 5-13 (L7->Y)	APRTLTVYLL	1351
	B8	B*0801	Steinlin	IVgp 586-593 Y1->F, Q5->	FLKDYQLL	1352
	B27	B*2705	LG2	R 60s	FRYNGLIHR	1353
	B35	B*3501	C1R, BVR	non-natural (B35CON2)	FPFKYAAAF	1354
	B35	B*3502	TISI	non-natural (B35CON2)	FPFKYAAAF	1355
	B35	B*3503	EHM	non-natural (B35CON2)	FPFKYAAAF	1356
	B44	B*4403	PITOUT	EF-1 G6->Y	AEMGKYSFY	1357
Mouse	B51		KAS116	non-natural (B35CON2)	FPFKYAAAF	1358
	B53	B*5301	AMAI	non-natural (B35CON2)	FPFKYAAAF	1359
	B54	B*5401	KT3	non-natural (B35CON2)	FPFKYAAAF	1360
	Cw4	Cw*0401	C1R	non-natural (C4CON1)	QYDDAVYKL	1361
	Cw6	Cw*0602	721.221 transfected	non-natural (C6CON1)	YRHDGNNVL	1362
	Cw7	Cw*0702	721.221 transfected	non-natural (C6CON1)	YRHDGNNVL	1363
	D <sup>b</sup>		EL4	Adenovirus E1A P7->Y	SGPSNTYPEI	1364
	K <sup>b</sup>		EL4	VSV NP 52-59	RGYVFQGL	1365
	D <sup>d</sup>		P815	HIV-IIIB ENV G4->Y	RGPYRAFTI	1366
	K <sup>d</sup>		P815	non-natural (KdCON1)	KFNPMKTYI	1367

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

L <sup>d</sup>		P815	HBVs 28-39	IPQSLDSYWTSL	1368
B. Class II binding assays					
Species	Antigen	Allele	Cell line	Radiolabeled peptide	
				Source	Sequence
Human	DR1	DRB1*0101	LG2	HA Y307-319	YPKYVVKQNTLKLAT
	DR2	DRB1*1501	L466.1	MBP 88-102Y	VVHFFKNIVTPRTPPY
	DR2	DRB1*1601	L242.5	non-natural (760.16)	YAAFAAAKTAFAAFA
	DR3	DRB1*0301	MAT	MT 65kD Y3-13	YKTIADFDEARR
	DR4w4	DRB1*0401	Preiss	non-natural (717.01)	YARFQSQTTLKQKT
	DR4w10	DRB1*0402	YAR	non-natural (717.10)	YARFQRQTTLKAAA
	DR4w14	DRB1*0404	BIN 40	non-natural (717.01)	YARFQSQTTLKQKT
	DR4w15	DRB1*0405	KT3	non-natural (717.01)	YARFQSQTTLKQKT
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843	QYIKANSKFIGITE
	DR8	DRB1*0802	OLL	Tet. tox. 830-843	QYIKANSKFIGITE
	DR8	DRB1*0803	LUY	Tet. tox. 830-843	QYIKANSKFIGITE
	DR9	DRB1*0901	HID	Tet. tox. 830-843	QYIKANSKFIGITE
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	QYIKANSKFIGITE
	DR12	DRB1*1201	Herluf	unknown eluted peptide	EALIHQLKINPYVLS
	DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A	QYIKANAKFIGITE
	DR51	DRB5*0101	GM3107 or L416.3	Tet. tox. 830-843	QYIKANAKFIGITE
	DR51	DRB5*0201	L255.1	HA 307-319	PKYVVKQNTLKLAT
	DR52	DRB3*0101	MAT	Tet. tox. 830-843	NGQIGNDPNRDIL
	DR53	DRB4*0101	L257.6	non-natural (717.01)	YARFQSQTTLKQKT
	DQ3.1	QA1*0301/DQB1*030	PF	non-natural (ROIV)	YAHAAHAAHAAHAAHAA
Mouse	IA <sup>b</sup>		DB27.4	non-natural (ROIV)	YAHAAHAAHAAHAAHAA
	IA <sup>d</sup>		A20	non-natural (ROIV)	YAHAAHAAHAAHAAHAA
	IA <sup>k</sup>		CH-12	HEL 46-61	YNTDGGSTDYGILQINSR
	IA <sup>s</sup>		LS102.9	non-natural (ROIV)	YAHAAHAAHAAHAAHAA
	IA <sup>u</sup>		91.7	non-natural (ROIV)	YAHAAHAAHAAHAAHAA
	IE <sup>d</sup>		A20	Lambda repressor 12-26	YLEDARRKKAIYEKKK
	IE <sup>k</sup>		CH-12	Lambda repressor 12-26	YLEDARRKKAIYEKKK
SEQ ID NO:					
					1369
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Table XXVI. Crossbinding of A2 supermotif peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound
p53.24	9	KLLPENNVL	1396	313	1955	--	1194	--	1
p53.25	11	LLPENNVLSP	1397	19	6.2	4.5	12	1702	4
p53.65	10	RMPEAAPV	1398	78	102	13	841	--	3
p53.65	9	RMPEAAPV	1399	119	23	22	70	--	4
p53.113	10	FLHSGTAKSV	1400	357	179	15	4625	--	3
p53.132	9	KMFCQLAKT	1401	333	33	18	106	--	4
p53.135	9	CQLAKTCPV	1402	208	43	143	90	--	4
p53.136	8	QLAKTCPV	1403	455	--	100	2643	1067	2
p53.164	9	KSQHMTVEV	1404	500	130	170	285	--	4
p53.187	11	GLAPPQHLIRV	1405	79	39	11	55	--	4
p53.193	11	HLIRVEGNLHV	1406	385	1387	83	1194	1778	2
p53.229	9	CTTHYNYM	1407	278	287	2564	561	181	3
p53.263	10	NLLGRNSFEV	1408	217	--	2500	881	--	1
p53.264	9	LLGRNSFEV	1409	85	358	37	206	--	4

-- indicates binding affinity = 10,000nM.

*added*

*146*



Table XXVIII. Crossbinding of A2 supermotif analogs

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound
p53.69	8	AAPPVAPA	1411	5000	1536	1177	1233	4706	0
p53.69L2V8	8	ALPPVAPV	1412	217	7167	500	285	67	4
p53.101	11	KTYQGSYGFRLL	1413	1786	896	--	514	615	0
p53.101L2V1	11	KLYQGSYGFRV	1414	81	48	24	116	--	4
p53.129	9	ALNKMFCQL	1415	735	391	19	73	--	3
p53.129V9	9	ALNKMFCQV	1416	75	165	7.7	15	--	4
p53.129B7V9	9	ALNKMFBQV	1417	192	391	23	49	--	4
p53.129	10	ALNKMFCQLA	1418	1316	1075	71	4625	--	1
p53.129V10	10	ALNKMFCQLV	1419	217	287	71	7400	--	3
p53.132	9	KMFCQLAKT	1420	333	33	18	106	--	4
p53.132V9	9	KMFCQLAKV	1421	33	8.4	7.7	15	--	4
p53.132B4V9	9	KMFBQLAKV	1422	125	13	9.1	37	8889	4
p53.132L2V9	9	KLFCQLAKV	1423	98	3.6	3.4	10	1270	4
p53.135	9	CQLAKTCPV	1424	208	43	143	90	--	4
p53.135L2	9	CLLAKTCPV	1425	125	506	67	370	--	3
p53.135B1B7	9	BQLAKTBPV	1426	102	71	15	67	--	4
p53.135B1L2I	9	BLLAKTBPV	1427	46	119	7.7	64	--	4
p53.139	9	KTCPVQLWV	1428	725	606	217	15	--	2
p53.139L2	9	KLCPVQLWV	1429	122	239	29	23	--	4
p53.139L2B3	9	KLBPVQLWV	1430	46	29	19	31	--	4
p53.149	9	STPPPGTRV	1431	909	1162	1031	--	129	1
p53.149M2	9	SMPPPGTRV	1432	172	215	13	425	667	4
p53.149L2	9	SLPPPGTRV	1433	122	226	13	9250	140	4
p53.164	9	KOSQHMTEV	1434	500	130	170	285	--	4
p53.164L2	9	KLQSHMTEV	1435	122	94	35	46	--	4
p53.216	10	VVVPYEPPEV	1436	617	1870	455	1194	--	1
p53.216L2	10	VLVPYEPPEV	1437	89	391	71	2056	--	3
p53.236	11	YMCNSSCMGGM	1438	667	391	67	974	5333	2
p53.236L2M1	11	YLCNSSCMGGV	1439	22	13	3.6	18	1569	4
p53.255	11	ITLEDSSGNLL	1440	1563	1265	2857	507	6667	0
p53.255L2V1	11	ILLEDSSGNLV	1441	33	123	71	206	--	4

-- indicates binding affinity = 10,000nM.

*Handwritten:* 148  
*Handwritten:* 6000, NW

Table XXIX. Immunogenicity of A2 supermotif analogs

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound	CTL Peptide <sup>1</sup>	CTL Wild-type	CTL Tumor
p53.69	8	AAPPVAPA	1442	5000	1536	1177	1233	4706	0			
p53.69L2V8	8	ALPPVAPV	1443	217	7167	500	285	67	4	2/4	1/3	0/3
p53.129	9	ALNKMFCQL	1444	735	391	19	73	-- <sup>2</sup>	3			
p53.129V9	9	ALNKMFCQV	1445	75	165	7.7	15	--	4	0/1		
p53.129B7V9	9	ALNKMFBQV	1446	192	391	23	49	--	4	2/4	0/3	0/2
p53.132	9	KMFCQLAKT	1447	333	33	18	106	--	4			
p53.132V9	9	KMFCQLAKV	1448	33	8.4	7.7	15	--	4	1/3	0/2	0/2
p53.132B4V9	9	KMFBQLAKV	1449	125	13	9.1	37	8889	4	5/5	0/4	0/4
p53.132L2V9	9	KLFCQLAKV	1450	98	3.6	3.4	9.5	1270	4	2/3	1/3	0/3
p53.139	9	KTCPVQLWV	1451	725	606	217	15	--	2			
p53.139L2	9	KLCPVQLWV	1452	122	239	29	23	--	4	2/5	2/3	1/3
p53.139L2B3	9	KLBPVQLWV	1453	45	29	19	31	--	4	3/4	2/3	1/2
p53.149	9	STPPGTRV	1454	909	1162	1031	--	129	1			
p53.149L2	9	SLPPGTRV	1455	122	226	13	9250	140	4	2/3	1/3	0/3
p53.149M2	9	SMPPGTRV	1456	172	215	13	425	667	4	2/4	2/4	2/4
p53.216	10	VVVPYEPPEV	1457	617	1870	455	1194	--	1			
p53.216L2	10	VLVPYEPPEV	1458	89	391	71	2056	--	3	1/1	1/1	
p53.255	11	ITLEDSSGNLL	1459	1563	1265	2857	507	6667	0			
p53.255L2V11	11	ILLEDSSGNLV	1460	33	123	71	206	--	4	1/3	0/3	0/2

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity = 10,000nM.

*add. 1*  
*can. m.*

**Table XXX. DR supertype primary binding**

Peptide	DR147 Algo Sum	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR147 Cross- binding
39.0307	2	GFRLGFLHSGTAKSV	1461	P53.108	3	5.4	89	3
39.0308	2	LNKMFCQLAKTCPVO	1462	P53.130	20	804	167	3
39.0309	2	MGGMNRRRPILTIITL	1463	P53.243	--	--	--	0
39.0310	2	RRPILTIITLEDSSG	1464	P53.248	5000	4500	--	0
39.0311	2	KRALPNNTSSSPQPK	1465	P53.305	--	--	--	0
39.0312	2	DGEYFTLQIRGRERF	1466	P53.324	125	--	--	1

-- indicates binding affinity =10,000nM.

*Added  
summary*

Table XXXI. DR supertype cross-binding

Peptide	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR2w2 $\beta$ 1 nM	DR2w2 $\beta$ 2 nM	DR6w1 9 nM	DR5w1 1 nM	DR8w2 nM	DR147 Binding	Broad Binding (5/8)
39.0307	GFRLGFLHSGTAKSV	1467	p53.108	2.6	5.4	89	253	167	76	100	29	3	8
39.0308	LNKMFCQLAKTCPV	1468	p53.130	20	804	167	5688	541	365	2500	1531	3	5

-- indicates binding affinity = 10,000nM.



**Table XXX. DR supertype primary binding**

Peptide	DR147 Algo Sum	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR147 Cross- binding
39.0307	2	GFRLGFLHSGTAKSV	1461	P53.108	3	5.4	89	3
39.0308	2	LNKMFCQLAKTCPVQ	1462	P53.130	20	804	167	3
39.0309	2	MGGMNRRPILTIITL	1463	P53.243	--	--	--	0
39.0310	2	RRPILTIITLEDSSG	1464	P53.248	5000	4500	--	0
39.0311	2	KRALPNNTSSSPQPK	1465	P53.305	--	--	--	0
39.0312	2	DGEYFTLQIRGRERF	1466	P53.324	125	--	--	1

-- indicates binding affinity =10,000nM.

Table XXXIII. HTL candidate peptides

Peptide	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w 4 nM	DR7 nM	DR3 nM	DR2w 2 $\beta$ 1 nM	DR2w 2 $\beta$ 2 nM	DR6w 1 nM	DR5w 1 nM	DR8w 2 nM	DR14 7 Bindin g	Broad Binding (5/8)	DR 3 Binder
39.0307	GFRLGFLHSGTAKSV	1485	p53.108	2.6	5.4	89	--	253	167	76	100	29	3	8	0
39.0308	LNKMFCQLAKTCPVQ	1486	p53.130	20	804	167	--	5688	541	365	2500	1531	3	5	0

-- indicates binding affinity = 10,000nM.